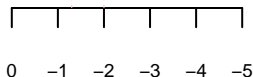


Oecy.Fem-Mal_difpos domain

Ala_racemase_N	p = 0.017 n = 1
Arginase	p = 0.017 n = 1
ATP-cone	p = 0.017 n = 1
CAF1A	p = 0.017 n = 1
dUTPase	p = 0.017 n = 1
eIF_4EBP	p = 0.017 n = 1
Glyco_hydro_2	p = 0.017 n = 1
Glyco_hydro_2_C	p = 0.017 n = 1
Glyco_hydro_2_N	p = 0.017 n = 1
Glyoxalase_4	p = 0.017 n = 1
HgmA	p = 0.017 n = 1
LRR_8	p = 0.017 n = 5
Mak16	p = 0.017 n = 1
MCM	p = 0.017 n = 2
MCM_N	p = 0.017 n = 2
MCM_OB	p = 0.017 n = 2
Methyltransf_4	p = 0.017 n = 1
Microtub_bind	p = 0.017 n = 1
NOC3p	p = 0.017 n = 1
NPR2	p = 0.017 n = 1
Phos_pyr_kin	p = 0.017 n = 1
Ribonuc_red_lgC	p = 0.017 n = 1
Ribonuc_red_lgN	p = 0.017 n = 1
Ribosomal_L20	p = 0.017 n = 1
SSF	p = 0.017 n = 2
TIR	p = 0.017 n = 2
Tma16	p = 0.017 n = 1
Cdc6_C	p = 0.0218 n = 1
CP2	p = 0.0218 n = 1
DNA_ligase_A_C	p = 0.0218 n = 1



log(p)

n = 72 genes | p adjust BH TRUE